



SEQUENCE LISTING

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<120> COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL
INTERACTION

<130> 89 DIV

<140> US 10/625,202

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<160> 2

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> Homo sapiens

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gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag	96
Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys	
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agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc	144
Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu	
35 40 45	

tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc	192
Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro	
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Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn	
65 70 75 80	
ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag	288
Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys	
85 90 95	
ctg cag gag atc tac cag gag ctg acc cag ctg aag gct gca gtg ggt	336
Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly	
100 105 110	
gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag ctg acc	384
Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
115 120 125	
cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag	432
Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
130 135 140	
gag atc tac cag gag ctg acc tgg ctg aag gct gca gtg ggt gag ctt	480
Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu	
145 150 155 160	
cca gag aaa tct aag atg cag gag atc tac cag gag ctg act cgg ctg	528
Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
165 170 175	
aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc	576
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile	
180 185 190	
tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag	624
Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
195 200 205	
aaa tct aag cag cag gag atc tac cag gag ctg acc cgg ctg aag gct	672
Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala	
210 215 220	
gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc tac cag	720
Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln	
225 230 235 240	
gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg tgc cac ccc tgt	768
Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys	
245 250 255	
ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac ttc atg tct aac	816
Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn	
260 265 270	
tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc aaa gaa gtg ggg	864
Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly	
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gcc cag ctc gtc gta atc aaa agt gct gag gag cag aac ttc cta cag 912
 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
 290 295 300
 ctg cag tct tcc aga agt aac cgc ttc acc tgg atg gga ctt tca gat 960
 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
 305 310 315 320
 cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc tca cct ctg ttg 1008
 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
 325 330 335
 ccc agc ttc aag cag tat tgg aac aga gga gag ccc aac aac gtt ggg 1056
 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
 340 345 350
 gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa 1104
 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
 355 360 365
 tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc 1152
 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
 370 375 380
 tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac 1200
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 20 25 30
 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
 35 40 45
 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
 50 55 60

Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
65 70 75 80

Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
85 90 95

Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
100 105 110

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
115 120 125

Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
130 135 140

Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
145 150 155 160

Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
165 170 175

Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
180 185 190

Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
195 200 205

Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
210 215 220

Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
225 230 235 240

Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
245 250 255

Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
260 265 270

Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
275 280 285

Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
 290 295 300

Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
 305 310 315 320

Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
 325 330 335

Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
 340 345 350

Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
 355 360 365

Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
 370 375 380

Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
 385 390 395 400

Pro Pro Pro Ala